



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/022,025
Source: OIPK
Date Processed by STIC: 10/25/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
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Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/022,025

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ✓ Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/022,025

DATE: 10/25/2002

TIME: 16:08:21

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Output Set: N:\CRF4\10252002\J022025.raw

5 <110> APPLICANT: Coleman, John R.

9 <120> TITLE OF INVENTION: Nucelic Acid Molecules and Polypeptides for Catabolism of
Absciscic

10 Acid

14 <130> FILE REFERENCE: 3310 0003

18 <140> CURRENT APPLICATION NUMBER: US 10/022,025

20 <141> CURRENT FILING DATE: 2001-12-13

24 <150> PRIOR APPLICATION NUMBER: US 60/254,819

26 <151> PRIOR FILING DATE: 2000-12-13

30 <160> NUMBER OF SEQ ID NOS: 8

34 <170> SOFTWARE: PatentIn version 3.0

38 <210> SEQ ID NO: 1

40 <211> LENGTH: 2009

42 <212> TYPE: DNA

44 <213> ORGANISM: Arabidopsis thaliana

48 <220> FEATURE:

50 <221> NAME/KEY: gene

52 <222> LOCATION: (1)..(2009)

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61 tatctctctc ttctcttcac ttactttgct ttgatccgcc atggctacga aactcgaaag 180
63 ctcccttaatc ttggcccttt tgtccaaatg cagcgttcta agccaaacca accttgccct 240
65 ctccctcctc gccgtcacia tcatctggct cgccatatct ctcttcttat ggacctatcc 300
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69 cggaaacggt attcccggtc caaaaaggctt ccctttgggt ggaagcatgt cactcatgtc 420
71 aagcactcta gtcaccgac gaatcgctga tgcagctgag aaattcggag ccaagaggct 480
73 catggctttc agcttaggag agactcgct gatcgctacg tgcaatcccg acgtagcgaa 540
75 agagattctg aatagcccgg tttttgctga tcgaccgggt aaagaatcgg ctactact 600
77 gatgtttaac agagcaattg gttttgcacc acacggtgtt tactggcgaa cgcttcgccg 660
79 tatcgcttcg aaccatctct ttagtataaa acaaatcaga agagccgaga cgcaacgacg 720
81 agtgatctca agccagatgg ttgagtttct tgaaaaacag agtagtaacg aacctgttt 780
83 tgttcgtgag ttgcttaaaaa cggcgctcgt taacaacatg atgtgctctg tattcgga 840
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87 tttgctcgga acgttgaatt ggactgatca ccttccttgg ctatcggagt ttgatcctca 960
89 aagactccgg tctagatggt ccacactcgt accaaaggta aaccggtttg tatcccggt 1020
91 tatatccgaa caccgtaatc aaaccggtga tttgcctcgt gatttcgtcg acgttttgct 1080
93 ctccctccat ggttcagata aattatccga cccggacata atcgccgttc tttgggtatg 1140
95 cacaccattt atttgattaa ttattcttaa ttatatttgt tgaaaattgc ttaggattat 1200
97 ttagattaaa acatgaaatt tgagactcaa tgtgacgtgt tgtggaataa ttaaagcatt 1260
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101 aagtaaaaaa tactaaaatt tttgagttat tattacagga gatgatattc agaggaacag 1380
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105 aatcaacggt acaaaacgag ctggatcaag tagtcgggaa atcaagagcc ctagatgaat 1500

Does Not Comply
Corrected Diskette NeededDoes Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/022,025

DATE: 10/25/2002

TIME: 16:08:21

Input Set : A:\ep.txt

Output Set: N:\CRF4\10252002\J022025.raw

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141 <222> LOCATION: (1)..(1593)
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148 1 5 10 15
150 tgc agc gtt cta agc caa acc aac ctt gcc ttc tcc ctc ctc gcc gtc 96
151 Cys Ser Val Leu Ser Gln Thr Asn Leu Ala Phe Ser Leu Leu Ala Val
152 20 25 30
154 aca atc atc tgg ctc gcc ata tct ctc ttc tta tgg acc tat ccc ggt 144
155 Thr Ile Ile Trp Leu Ala Ile Ser Leu Phe Leu Trp Thr Tyr Pro Gly
156 35 40 45
158 gga cct gct tgg ggg aaa tac ctc ttc ggc cgg tta ata tcc ggt tca 192
159 Gly Pro Ala Trp Gly Lys Tyr Leu Phe Gly Arg Leu Ile Ser Gly Ser
160 50 55 60
162 tac aaa acc gga aac gtt att ccc ggt cca aaa ggc ttc cct ttg gtt 240
163 Tyr Lys Thr Gly Asn Val Ile Pro Gly Pro Lys Gly Phe Pro Leu Val
164 65 70 75 80
166 gga agc atg tca ctc atg tca agc act cta gct cac cga cga atc gct 288
167 Gly Ser Met Ser Leu Met Ser Ser Thr Leu Ala His Arg Arg Ile Ala
168 85 90 95
170 gat gca gct gag aaa ttc gga gcc aag agg ctc atg gct ttc agc tta 336
171 Asp Ala Ala Glu Lys Phe Gly Ala Lys Arg Leu Met Ala Phe Ser Leu
172 100 105 110
174 gga gag act cgc gtg atc gtc acg tgc aat ccc gac gta gcg aaa gag 384
175 Gly Glu Thr Arg Val Ile Val Thr Cys Asn Pro Asp Val Ala Lys Glu
176 115 120 125
178 att ctg aat agc ccg gtt ttt gct gat cga ccg gtt aaa gaa tcg gct 432
179 Ile Leu Asn Ser Pro Val Phe Ala Asp Arg Pro Val Lys Glu Ser Ala
180 130 135 140
182 tac tca ctg atg ttt aac aga gca att ggt ttt gca cca cac ggt gtt 480
183 Tyr Ser Leu Met Phe Asn Arg Ala Ile Gly Phe Ala Pro His Gly Val
184 145 150 155 160
186 tac tgg cga acg ctt cgc cgt atc gct tcg aac cat ctc ttt agt aca 528
187 Tyr Trp Arg Thr Leu Arg Arg Ile Ala Ser Asn His Leu Phe Ser Thr

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191	Lys Gln Ile Arg Arg Ala Glu Thr Gln Arg Arg Val Ile Ser Ser Gln			
192	180 185 190			
194	atg gtt gag ttt ctt gaa aaa cag agt agt aac gaa ccc tgt ttt gtt	624		
195	Met Val Glu Phe Leu Glu Lys Gln Ser Ser Asn Glu Pro Cys Phe Val			
196	195 200 205			
199	cgt gag ttg ctt aaa acg gcg tcg ctt aac aac atg atg tgc tct gta	672		
200	Arg Glu Leu Leu Lys Thr Ala Ser Leu Asn Asn Met Met Cys Ser Val			
201	210 215 220			
203	ttc gga caa gag tat gag ctt gaa aaa aac cat gtt gag tta cgt gaa	720		
204	Phe Gly Gln Glu Tyr Glu Leu Glu Lys Asn His Val Glu Leu Arg Glu			
205	225 230 235 240			
207	atg gtc gaa gaa ggt tat gat ttg ctc gga acg ttg aat tgg act gat	768		
208	Met Val Glu Glu Gly Tyr Asp Leu Leu Gly Thr Leu Asn Trp Thr Asp			
209	245 250 255			
211	cac ctt cct tgg cta tcg gag ttt gat cct caa aga ctc cgg tct aga	816		
212	His Leu Pro Trp Leu Ser Glu Phe Asp Pro Gln Arg Leu Arg Ser Arg			
213	260 265 270			
215	tgt tcc aca ctc gta cca aag gta aac cgg ttt gta tcc cgg att ata	864		
216	Cys Ser Thr Leu Val Pro Lys Val Asn Arg Phe Val Ser Arg Ile Ile			
217	275 280 285			
219	tcc gaa cac cgt aat caa acc ggt gat ttg cct cgt gat ttc gtc gac	912		
220	Ser Glu His Arg Asn Gln Thr Gly Asp Leu Pro Arg Asp Phe Val Asp			
221	290 295 300			
223	gtt ttg ctc tcc ctc cat ggt tca gat aaa tta tcc gac ccg gac ata	960		
224	Val Leu Leu Ser Leu His Gly Ser Asp Lys Leu Ser Asp Pro Asp Ile			
225	305 310 315 320			
227	atc gcc gtt ctt tgg gag atg ata ttc aga gga aca gac aca gtt gcg	1008		
228	Ile Ala Val Leu Trp Glu Met Ile Phe Arg Gly Thr Asp Thr Val Ala			
229	325 330 335			
231	gtc tta atc gag tgg atc ctc gct agg atg gtc ctt cat cca gat atg	1056		
232	Val Leu Ile Glu Trp Ile Leu Ala Arg Met Val Leu His Pro Asp Met			
233	340 345 350			
235	caa tca acg gta caa aac gag ctg gat caa gta gtc ggg aaa tca aga	1104		
236	Gln Ser Thr Val Gln Asn Glu Leu Asp Gln Val Val Gly Lys Ser Arg			
237	355 360 365			
239	gcc cta gat gaa tct gac ttg gct tca ctt cca tat cta acg gct gtg	1152		
240	Ala Leu Asp Glu Ser Asp Leu Ala Ser Leu Pro Tyr Leu Thr Ala Val			
241	370 375 380			
243	gtg aaa gaa gta ttg agg ctt cat cct cca ggc cca ctt cta tca tgg	1200		
244	Val Lys Glu Val Leu Arg Leu His Pro Pro Gly Pro Leu Leu Ser Trp			
245	385 390 395 400			
247	gcc cgt ttg gcc ata aca gac acg atc gtt gat ggt cgt ctt gtt ccg	1248		
248	Ala Arg Leu Ala Ile Thr Asp Thr Ile Val Asp Gly Arg Leu Val Pro			
249	405 410 415			
251	gca ggg acc aca gca atg gtg aac atg tgg gcc gta tcg cat gat cca	1296		
252	Ala Gly Thr Thr Ala Met Val Asn Met Trp Ala Val Ser His Asp Pro			
253	420 425 430			

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Output Set: N:\CRF4\10252002\J022025.raw

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259 aaa gaa ggt gag gtg gag ttt tcg gtt ctt ggg tcg gat ttg aga ctt      1392
260 Lys Glu Gly Glu Val Glu Phe Ser Val Leu Gly Ser Asp Leu Arg Leu
261          450                      455                      460
263 gca cct ttc ggg tcg ggt cgt cgg att tgc ccc ggg aag aat ctt ggt      1440
265 Ala Pro Phe Gly Ser Gly Arg Arg Ile Cys Pro Gly Lys Asn Leu Gly
266 465          470                      475                      480
268 ttt act acc gtt atg ttt tgg acg gcg atg atg tta cat gag ttt gaa      1488
269 Phe Thr Thr Val Met Phe Trp Thr Ala Met Met Leu His Glu Phe Glu
270          485                      490                      495
272 tgg gga ccg tcc gat ggt aac ggc gtt gac tta tct gag aaa ctg agg      1536
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274          500                      505                      510
276 ctt tct tgc gag atg gct aat cct ctt cct gct aaa ttg cgc cgt agg      1584
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282          530
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287 <211> LENGTH: 530
289 <212> TYPE: PRT
291 <213> ORGANISM: Arabidopsis thaliana
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305 Thr Ile Ile Trp Leu Ala Ile Ser Leu Phe Leu Trp Thr Tyr Pro Gly
306          35          40          45
309 Gly Pro Ala Trp Gly Lys Tyr Leu Phe Gly Arg Leu Ile Ser Gly Ser
310          50          55          60
313 Tyr Lys Thr Gly Asn Val Ile Pro Gly Pro Lys Gly Phe Pro Leu Val
314 65          70          75          80
317 Gly Ser Met Ser Leu Met Ser Ser Thr Leu Ala His Arg Arg Ile Ala
318          85          90          95
321 Asp Ala Ala Glu Lys Phe Gly Ala Lys Arg Leu Met Ala Phe Ser Leu
322          100         105         110
325 Gly Glu Thr Arg Val Ile Val Thr Cys Asn Pro Asp Val Ala Lys Glu
326          115         120         125
329 Ile Leu Asn Ser Pro Val Phe Ala Asp Arg Pro Val Lys Glu Ser Ala
331          130         135         140
334 Tyr Ser Leu Met Phe Asn Arg Ala Ile Gly Phe Ala Pro His Gly Val
335 145          150         155         160
338 Tyr Trp Arg Thr Leu Arg Arg Ile Ala Ser Asn His Leu Phe Ser Thr
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342 Lys Gln Ile Arg Arg Ala Glu Thr Gln Arg Arg Val Ile Ser Ser Gln

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Input Set : A:\ep.txt

Output Set: N:\CRF4\10252002\J022025.raw

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351          210          215          220
354 Phe Gly Gln Glu Tyr Glu Leu Glu Lys Asn His Val Glu Leu Arg Glu
355 225          230          235          240
358 Met Val Glu Glu Gly Tyr Asp Leu Leu Gly Thr Leu Asn Trp Thr Asp
359          245          250          255
362 His Leu Pro Trp Leu Ser Glu Phe Asp Pro Gln Arg Leu Arg Ser Arg
363          260          265          270
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371          290          295          300
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375 305          310          315          320
378 Ile Ala Val Leu Trp Glu Met Ile Phe Arg Gly Thr Asp Thr Val Ala
379          325          330          335
382 Val Leu Ile Glu Trp Ile Leu Ala Arg Met Val Leu His Pro Asp Met
383          340          345          350
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387          355          360          365
390 Ala Leu Asp Glu Ser Asp Leu Ala Ser Leu Pro Tyr Leu Thr Ala Val
391          370          375          380
394 Val Lys Glu Val Leu Arg Leu His Pro Pro Gly Pro Leu Leu Ser Trp
395 385          390          395          400
398 Ala Arg Leu Ala Ile Thr Asp Thr Ile Val Asp Gly Arg Leu Val Pro
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402 Ala Gly Thr Thr Ala Met Val Asn Met Trp Ala Val Ser His Asp Pro
403          420          425          430
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407          435          440          445
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411          450          455          460
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415 465          470          475          480
418 Phe Thr Thr Val Met Phe Trp Thr Ala Met Met Leu His Glu Phe Glu
419          485          490          495
422 Trp Gly Pro Ser Asp Gly Asn Gly Val Asp Leu Ser Glu Lys Leu Arg
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431          530
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436 <211> LENGTH: 15
438 <212> TYPE: DNA
440 <213> ORGANISM: synthetic construct

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see item 10 on Error Summary sheet

*Please correct this error
in subsequent sequences.*

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/022,025

DATE: 10/25/2002

TIME: 16:08:22

Input Set : A:\ep.txt

Output Set: N:\CRF4\10252002\J022025.raw